



SEQUENCE LISTING

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<120> PYK2 CRYSTAL STRUCTURE AND USES

<130> 039363/1202

<140> 10/789,818
<141> 2004-02-27

<150> 60/451,101
<151> 2003-02-28

<160> 25

<170> PatentIn Ver. 3.2

<210> 1
<211> 272
<212> PRT
<213> Homo sapiens

<400> 1
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1 5 10 15
Phe Gly Glu Val Tyr Glu Gly Val Tyr Thr Asn His Lys Gly Glu Lys
20 25 30
Ile Asn Val Ala Val Lys Thr Cys Lys Lys Asp Cys Thr Leu Asp Asn
35 40 45
Lys Glu Lys Phe Met Ser Glu Ala Val Ile Met Lys Asn Leu Asp His
50 55 60
Pro His Ile Val Lys Leu Ile Gly Ile Ile Glu Glu Glu Pro Thr Trp
65 70 75 80
Ile Ile Met Glu Leu Tyr Pro Tyr Gly Glu Leu Gly His Tyr Leu Glu
85 90 95
Arg Asn Lys Asn Ser Leu Lys Val Leu Thr Leu Val Leu Tyr Ser Leu
100 105 110
Gln Ile Cys Lys Ala Met Ala Tyr Leu Glu Ser Ile Asn Cys Val His
115 120 125
Arg Asp Ile Ala Val Arg Asn Ile Leu Val Ala Ser Pro Glu Cys Val
130 135 140
Lys Leu Gly Asp Phe Gly Leu Ser Arg Tyr Ile Glu Asp Glu Asp Tyr
145 150 155 160

Tyr Lys Ala Ser Val Thr Arg Leu Pro Ile Lys Trp Met Ser Pro Glu
 165 170 175
 Ser Ile Asn Phe Arg Arg Phe Thr Thr Ala Ser Asp Val Trp Met Phe
 180 185 190
 Ala Val Cys Met Trp Glu Ile Leu Ser Phe Gly Lys Gln Pro Phe Phe
 195 200 205
 Trp Leu Glu Asn Lys Asp Val Ile Gly Val Leu Glu Lys Gly Asp Arg
 210 215 220
 Leu Pro Lys Pro Asp Leu Cys Pro Pro Val Leu Tyr Thr Leu Met Thr
 225 230 235 240
 Arg Cys Trp Asp Tyr Asp Pro Ser Asp Arg Pro Arg Phe Thr Glu Leu
 245 250 255
 Val Cys Ser Leu Ser Asp Val Tyr Gln Met Glu Lys Asp Ile Ala Met
 260 265 270

<210> 2
 <211> 293
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 pET15S protein containing PYK2

<400> 2
 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15
 Arg Gly Ser His Met Ile Ala Arg Glu Asp Val Val Leu Asn Arg Ile
 20 25 30
 Leu Gly Glu Gly Phe Phe Gly Glu Val Tyr Glu Gly Val Tyr Thr Asn
 35 40 45
 His Lys Gly Glu Lys Ile Asn Val Ala Val Lys Thr Cys Lys Lys Asp
 50 55 60
 Cys Thr Leu Asp Asn Lys Glu Lys Phe Met Ser Glu Ala Val Ile Met
 65 70 75 80
 Lys Asn Leu Asp His Pro His Ile Val Lys Leu Ile Gly Ile Ile Glu
 85 90 95
 Glu Glu Pro Thr Trp Ile Ile Met Glu Leu Tyr Pro Tyr Gly Glu Leu
 100 105 110
 Gly His Tyr Leu Glu Arg Asn Lys Asn Ser Leu Lys Val Leu Thr Leu
 115 120 125

Val Leu Tyr Ser Leu Gln Ile Cys Lys Ala Met Ala Tyr Leu Glu Ser
 130 135 140
 Ile Asn Cys Val His Arg Asp Ile Ala Val Arg Asn Ile Leu Val Ala
 145 150 155 160
 Ser Pro Glu Cys Val Lys Leu Gly Asp Phe Gly Leu Ser Arg Tyr Ile
 165 170 175
 Glu Asp Glu Asp Tyr Tyr Lys Ala Ser Val Thr Arg Leu Pro Ile Lys
 180 185 190
 Trp Met Ser Pro Glu Ser Ile Asn Phe Arg Arg Phe Thr Thr Ala Ser
 195 200 205
 Asp Val Trp Met Phe Ala Val Cys Met Trp Glu Ile Leu Ser Phe Gly
 210 215 220
 Lys Gln Pro Phe Phe Trp Leu Glu Asn Lys Asp Val Ile Gly Val Leu
 225 230 235 240
 Glu Lys Gly Asp Arg Leu Pro Lys Pro Asp Leu Cys Pro Pro Val Leu
 245 250 255
 Tyr Thr Leu Met Thr Arg Cys Trp Asp Tyr Asp Pro Ser Asp Arg Pro
 260 265 270
 Arg Phe Thr Glu Leu Val Cys Ser Leu Ser Asp Val Tyr Gln Met Glu
 275 280 285
 Lys Asp Ile Ala Met
 290

<210> 3
 <211> 816
 <212> DNA
 <213> Homo sapiens

<400> 3
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 tatgaagggtg tctacacaaa tcacaaaggg gagaaaatca atgtagctgt caagacctgc 120
 aagaaagact gcactctgga caacaaggag aagttcatga gcgaggcagt gatcatgaag 180
 aacctcgacc acccgacat cgtgaagctg atcggcata ttgaagagga gcccacctgg 240
 atcatcatgg aattgtatcc ctatggggag ctgggccact acctggagcg gaacaagaac 300
 tccctgaagg tgctcaccct cgtgctgtac tctactgcaga tatgcaaagc catggcctac 360
 ctggagagca tcaactgcgt gcacagggac attgctgtcc ggaacatcct ggtggcctcc 420
 cctgagtgtg tgaagctggg ggactttggg ctttcccggt acattgagga cgaggactat 480
 tacaaagcct ctgtgactcg tctccccatc aaatggatgt ccccagagtc cattaacttc 540
 cgacgcttca cgacagccag tgacgtctgg atgttcgccg tgtgcatgtg ggagatcctg 600
 agctttggga agcagccctt cttctggctg gagaacaagg atgtcatcgg ggtgctggag 660
 aaaggagacc ggctgccccaa gcctgatctc tgtccaccgg tcctttatac cctcatgacc 720
 cgctgctggg actacgaccc cagtgaaccg ccccgcttca ccgagctggg gtgcagcctc 780
 agtgacgttt atcagatgga gaaggacatt gccatg 816

<210> 4
 <211> 1050
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 pET15S nucleotide sequence

<400> 4
 tctagaaata attttgttta actttaagaa ggagatatac catgggcagc agccatcatc 60
 atcatcatca cagcagcggc ctggtgccgc gcggcagcca tatgattgcc cgtgaagatg 120
 tggctcctgaa tcgtattctt ggggaaggct tttttgggga ggtctatgaa ggtgtctaca 180
 caaatcacia aggggagaaa atcaatgtag ctgtcaagac ctgcaagaaa gactgcactc 240
 tggacaacaa ggagaagtgc atgagcagag cagtgatcat gaagaacctc gaccacccgc 300
 acatcgtgaa gctgatcggc atcattgaag aggagcccac ctggatcatc atggaattgt 360
 atccctatgg ggagctgggc cactacctgg agcggaaaca gaactccctg aaggtgctca 420
 ccctcgtgct gtactcactg cagatatgca aagccatggc ctacctggag agcatcaact 480
 gcgtgcacag ggacattgct gtccggaaca tcctgggtggc ctcccctgag tgtgtgaagc 540
 tgggggactt tggctcttcc cggtacattg aggacgagga ctattacaaa gcctctgtga 600
 ctcgtctccc catcaaattg atgtcccag agtcattaa cttccgacgc ttcacgacag 660
 ccagtgcagt ctggatgttc gccgtgtgca tgtgggagat cctgagcttt gggaagcagc 720
 ccttcttctg gctggagaac aaggatgtca tcggggtgct ggagaaagga gaccggctgc 780
 ccaagcctga tctctgtcca ccggtccttt ataccctcat gaccgctgc tgggactacg 840
 accccagtga ccggccccgc ttcaccgagc tgggtgtgag cctcagtgac gtttatcaga 900
 tggagaagga cattgccatg taggtcgact agagcctgca gtctcgacca tcatcatcat 960
 catcattaat aaaagggcga attccagcac actggcggcc gttactagtg gatccggctg 1020
 ctaacaaagc ccgaaaggaa gctgagttgg 1050

<210> 5
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 5
 tccacagcat atgattgccc gtgaagatgt ggt 33

<210> 6
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 6
 ctctcgtcga cctacatggc aatgtccttc tcca 34

<210> 7
 <211> 391

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (108)..(170)

<220>

<223> Description of Artificial Sequence: Synthetic
pET15S multi-cloning site nucleotide sequence

<400> 7

agatctcgat cccgcgaaat taatacgact cactataggg gaattgtgag cggataacaa 60

ttcccctcta gaaataattt tgtttaactt taagaaggag atatacc atg ggc agc 116
Met Gly Ser
1

agc cat cat cat cat cat cac agc agc ggc ctg gtg ccg cgc ggc agc 164
Ser His His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser
5 10 15

cat atg ggatccgga ttcaaaggcc tacgtcgact agagcctgca gtctcgacca 220
His Met
20

tcatcatcat catcattaat aaaagggcga attccagcac actggcggcc gttactagtg 280

gatccggctg ctaacaaagc ccgaaaggaa gctgagttgg ctgctgccac cgctgagcaa 340

taactagcat aacccttgg ggcctctaaa cgggtcttga ggggtttttt g 391

<210> 8

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
pET15S multi-cloning site peptide sequence

<400> 8

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
1 5 10 15

Arg Gly Ser His Met
20

<210> 9

<211> 310

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: FAK tyrosine kinase
sequence

<400> 9

Glu	Ile	Gln	Arg	Glu	Arg	Ile	Glu	Leu	Gly	Arg	Cys	Ile	Gly	Glu	Gly	1	5	10	15
Gln	Phe	Gly	Asp	Val	His	Gln	Gly	Ile	Tyr	Met	Ser	Pro	Glu	Asn	Pro	20	25	30	
Ala	Leu	Ala	Val	Ala	Ile	Lys	Thr	Cys	Lys	Asn	Cys	Thr	Ser	Asp	Ser	35	40	45	
Val	Arg	Glu	Lys	Phe	Leu	Gln	Glu	Ala	Cys	His	Tyr	Thr	Ser	Leu	His	50	55	60	
Trp	Asn	Trp	Cys	Arg	Tyr	Ile	Ser	Asp	Pro	Asn	Val	Asp	Ala	Cys	Pro	65	70	75	80
Asp	Pro	Arg	Asn	Ala	Glu	Leu	Thr	Met	Arg	Gln	Phe	Asp	His	Pro	His	85	90	95	
Ile	Val	Lys	Leu	Ile	Gly	Val	Ile	Thr	Glu	Asn	Pro	Val	Trp	Ile	Ile	100	105	110	
Met	Glu	Leu	Cys	Thr	Leu	Gly	Glu	Leu	Arg	Ser	Phe	Leu	Gln	Val	Arg	115	120	125	
Lys	Tyr	Ser	Leu	Asp	Leu	Ala	Ser	Leu	Ile	Leu	Tyr	Ala	Tyr	Gln	Leu	130	135	140	
Ser	Thr	Ala	Leu	Ala	Tyr	Leu	Glu	Ser	Lys	Arg	Phe	Val	His	Arg	Asp	145	150	155	160
Ile	Ala	Ala	Arg	Asn	Val	Leu	Val	Ser	Ser	Asn	Asp	Cys	Val	Lys	Leu	165	170	175	
Gly	Asp	Phe	Gly	Leu	Ser	Arg	Tyr	Met	Glu	Asp	Ser	Thr	Tyr	Tyr	Lys	180	185	190	
Ala	Ser	Lys	Gly	Lys	Leu	Pro	Ile	Lys	Trp	Met	Ala	Pro	Glu	Ser	Ile	195	200	205	
Asn	Phe	Arg	Arg	Phe	Thr	Ser	Ala	Ser	Asp	Val	Trp	Met	Phe	Gly	Val	210	215	220	
Cys	Met	Trp	Glu	Ile	Leu	Met	His	Gly	Val	Lys	Pro	Phe	Gln	Gly	Val	225	230	235	240
Lys	Asn	Asn	Asp	Val	Ile	Gly	Arg	Ile	Glu	Asn	Gly	Glu	Arg	Leu	Pro	245	250	255	
Met	Pro	Pro	Asn	Cys	Pro	Pro	Thr	Leu	Tyr	Ser	Leu	Met	Thr	Lys	Cys	260	265	270	

Trp Ala Tyr Asp Pro Ser Arg Arg Pro Arg Phe Thr Glu Leu Lys Ala
 275 280 285

Gln Leu Ser Thr Ile Leu Glu Glu Glu Lys Ala Gln Gln Glu Glu Arg
 290 295 300

Met Arg Met Glu Ser Arg
 305 310

<210> 10

<211> 273

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: SRC tyrosine kinase
 sequence

<400> 10

Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly
 1 5 10 15

Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Arg Val
 20 25 30

Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Ser Pro Glu Ala Phe Leu
 35 40 45

Gln Glu Ala Gln Val Met Lys Lys Leu Arg His Glu Lys Leu Val Gln
 50 55 60

Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Tyr
 65 70 75 80

Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys Gly Glu Thr Gly Lys
 85 90 95

Tyr Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Ser
 100 105 110

Gly Met Ala Tyr Val Glu Arg Met Asn Tyr Val His Arg Asp Leu Arg
 115 120 125

Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Val Ala Asp
 130 135 140

Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln
 145 150 155 160

Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr
 165 170 175

Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu
 180 185 190

Thr Glu Leu Thr Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn
 195 200 205

Arg Glu Val Leu Asp Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro
 210 215 220

Pro Glu Cys Pro Glu Ser Leu His Asp Leu Met Cys Gln Cys Trp Arg
 225 230 235 240

Lys Glu Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ala Phe Leu
 245 250 255

Glu Asp Tyr Phe Thr Ser Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn
 260 265 270

Leu

<210> 11

<211> 271

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: HCK tyrosine kinase
 sequence

<400> 11

Glu Ile Pro Arg Glu Ser Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly
 1 5 10 15

Gln Phe Gly Glu Val Trp Met Ala Thr Tyr Asn Lys His Thr Lys Val
 20 25 30

Ala Val Lys Thr Met Lys Pro Gly Ser Met Ser Val Glu Ala Phe Leu
 35 40 45

Ala Glu Ala Asn Val Met Lys Thr Leu Gln His Asp Lys Leu Val Lys
 50 55 60

Leu His Ala Val Val Thr Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe
 65 70 75 80

Met Ala Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser
 85 90 95

Lys Gln Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu
 100 105 110

Gly Met Ala Phe Ile Glu Gln Arg Asn Tyr Ile His Arg Asp Leu Arg
 115 120 125

Ala Ala Asn Ile Leu Val Ser Ala Ser Leu Val Cys Lys Ile Ala Asp
 130 135 140

Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu
 145 150 155 160
 Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe
 165 170 175
 Gly Ser Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu
 180 185 190
 Met Glu Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn
 195 200 205
 Pro Glu Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro
 210 215 220
 Glu Asn Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys
 225 230 235 240
 Asn Arg Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu
 245 250 255
 Asp Asp Phe Tyr Thr Ala Thr Glu Ser Gln Tyr Glu Glu Ile Pro
 260 265 270

<210> 12

<211> 263

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: LCK tyrosine kinase
sequence

<400> 12

Glu Val Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly
 1 5 10 15
 Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val
 20 25 30
 Ala Val Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu
 35 40 45
 Ala Glu Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg
 50 55 60
 Leu Tyr Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Thr Glu Tyr
 65 70 75 80
 Met Glu Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile
 85 90 95
 Lys Leu Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu
 100 105 110

Gly Met Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg
 115 120 125
 Ala Ala Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp
 130 135 140
 Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu
 145 150 155 160
 Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr
 165 170 175
 Gly Thr Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu
 180 185 190
 Thr Glu Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn
 195 200 205
 Pro Glu Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro
 210 215 220
 Asp Asn Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys
 225 230 235 240
 Glu Arg Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu
 245 250 255
 Glu Asp Phe Phe Thr Ala Thr
 260

<210> 13

<211> 263

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: ABL1 tyrosine kinase
sequence

<400> 13

Glu Met Glu Arg Thr Asp Ile Thr Met Lys His Lys Leu Gly Gly Gly
 1 5 10 15
 Gln Tyr Gly Glu Val Tyr Glu Gly Val Trp Lys Lys Tyr Ser Leu Thr
 20 25 30
 Val Ala Val Lys Thr Leu Lys Glu Asp Thr Met Glu Val Glu Glu Phe
 35 40 45
 Leu Lys Glu Ala Ala Val Met Lys Glu Ile Lys His Pro Asn Leu Val
 50 55 60
 Gln Leu Leu Gly Val Cys Thr Arg Glu Pro Pro Phe Tyr Ile Ile Thr
 65 70 75 80

Glu Phe Met Thr Tyr Gly Asn Leu Leu Asp Tyr Leu Arg Glu Cys Asn
 85 90 95
 Arg Gln Glu Val Ser Ala Val Val Leu Leu Tyr Met Ala Thr Gln Ile
 100 105 110
 Ser Ser Ala Met Glu Tyr Leu Glu Lys Lys Asn Phe Ile His Arg Asp
 115 120 125
 Leu Ala Ala Arg Asn Cys Leu Val Gly Glu Asn His Leu Val Lys Val
 130 135 140
 Ala Asp Phe Gly Leu Ser Arg Leu Met Thr Gly Asp Thr Tyr Thr Ala
 145 150 155 160
 His Ala Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ser Leu
 165 170 175
 Ala Tyr Asn Lys Phe Ser Ile Lys Ser Asp Val Trp Ala Phe Gly Val
 180 185 190
 Leu Leu Trp Glu Ile Ala Thr Tyr Gly Met Ser Pro Tyr Pro Gly Ile
 195 200 205
 Asp Leu Ser Gln Val Tyr Glu Leu Leu Glu Lys Asp Tyr Arg Met Glu
 210 215 220
 Arg Pro Glu Gly Cys Pro Glu Lys Val Tyr Glu Leu Met Arg Ala Cys
 225 230 235 240
 Trp Gln Trp Asn Pro Ser Asp Arg Pro Ser Phe Ala Glu Ile His Gln
 245 250 255
 Ala Phe Glu Thr Met Phe Gln
 260

<210> 14

<211> 260

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: CSK tyrosine kinase
sequence

<400> 14

Ala Leu Asn Met Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly
 1 5 10 15
 Glu Phe Gly Asp Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala
 20 25 30
 Val Lys Cys Ile Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu
 35 40 45

Ala Ser Val Met Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu
 50 55 60
 Gly Val Ile Val Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr
 65 70 75 80
 Met Ala Lys Gly Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser
 85 90 95
 Val Leu Gly Gly Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu
 100 105 110
 Ala Met Glu Tyr Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala
 115 120 125
 Ala Arg Asn Val Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp
 130 135 140
 Phe Gly Leu Thr Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu
 145 150 155 160
 Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser
 165 170 175
 Thr Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr
 180 185 190
 Ser Phe Gly Arg Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val
 195 200 205
 Pro Arg Val Glu Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro
 210 215 220
 Pro Ala Val Tyr Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala
 225 230 235 240
 Met Arg Pro Ser Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys
 245 250 255
 Thr His Glu Leu
 260

<210> 15

<211> 295

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: TEK tyrosine kinase
sequence

<400> 15

Val Leu Asp Trp Asn Asp Ile Lys Phe Gln Asp Val Ile Gly Glu Gly
 1 5 10 15

Asn Phe Gly Gln Val Leu Lys Ala Arg Ile Lys Lys Asp Gly Leu Arg
 20 25 30
 Met Asp Ala Ala Ile Lys Arg Met Lys Glu Tyr Ala Ser Lys Asp Asp
 35 40 45
 His Arg Asp Phe Ala Gly Glu Leu Glu Val Leu Cys Lys Leu Gly His
 50 55 60
 His Pro Asn Ile Ile Asn Leu Leu Gly Ala Cys Glu His Arg Gly Tyr
 65 70 75 80
 Leu Tyr Leu Ala Ile Glu Tyr Ala Pro His Gly Asn Leu Leu Asp Phe
 85 90 95
 Leu Arg Lys Ser Arg Val Leu Glu Thr Asp Pro Ala Phe Ala Ile Ala
 100 105 110
 Asn Ser Thr Ala Ser Thr Leu Ser Ser Gln Gln Leu Leu His Phe Ala
 115 120 125
 Ala Asp Val Ala Arg Gly Met Asp Tyr Leu Ser Gln Lys Gln Phe Ile
 130 135 140
 His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Gly Glu Asn Tyr Val
 145 150 155 160
 Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Gly Gln Glu Val Tyr Val
 165 170 175
 Lys Lys Thr Met Gly Arg Leu Pro Val Arg Trp Met Ala Ile Glu Ser
 180 185 190
 Leu Asn Tyr Ser Val Tyr Thr Thr Asn Ser Asp Val Trp Ser Tyr Gly
 195 200 205
 Val Leu Leu Trp Glu Ile Val Ser Leu Gly Gly Thr Pro Tyr Cys Gly
 210 215 220
 Met Thr Cys Ala Glu Leu Tyr Glu Lys Leu Pro Gln Gly Tyr Arg Leu
 225 230 235 240
 Glu Lys Pro Leu Asn Cys Asp Asp Glu Val Tyr Asp Leu Met Arg Gln
 245 250 255
 Cys Trp Arg Glu Lys Pro Tyr Glu Arg Pro Ser Phe Ala Gln Ile Leu
 260 265 270
 Val Ser Leu Asn Arg Met Leu Glu Glu Arg Lys Thr Tyr Val Asn Thr
 275 280 285
 Thr Leu Tyr Glu Lys Phe Thr
 290 295

<210> 16

<211> 291

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: KDR tyrosine kinase
sequence

<400> 16

Glu	Phe	Pro	Arg	Asp	Arg	Leu	Lys	Leu	Gly	Lys	Pro	Leu	Gly	Arg	Gly	1	5	10	15
Ala	Phe	Gly	Gln	Val	Ile	Glu	Ala	Asp	Ala	Phe	Gly	Ile	Asp	Lys	Thr	20	25	30	
Ala	Thr	Cys	Arg	Thr	Val	Ala	Val	Lys	Met	Leu	Lys	Glu	Gly	Ala	Thr	35	40	45	
His	Ser	Glu	His	Arg	Ala	Leu	Met	Ser	Glu	Leu	Lys	Ile	Leu	Ile	His	50	55	60	
Ile	Gly	His	His	Leu	Asn	Val	Val	Asn	Leu	Leu	Gly	Ala	Cys	Thr	Lys	65	70	75	80
Pro	Gly	Gly	Pro	Leu	Met	Val	Ile	Val	Glu	Phe	Cys	Lys	Phe	Gly	Asn	85	90	95	
Leu	Ser	Thr	Tyr	Leu	Arg	Ser	Lys	Arg	Asn	Glu	Phe	Val	Pro	Tyr	Lys	100	105	110	
Val	Ala	Pro	Glu	Asp	Leu	Tyr	Lys	Asp	Phe	Leu	Thr	Leu	Glu	His	Leu	115	120	125	
Ile	Cys	Tyr	Ser	Phe	Gln	Val	Ala	Lys	Gly	Met	Glu	Phe	Leu	Ala	Ser	130	135	140	
Arg	Lys	Cys	Ile	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Leu	Ser	145	150	155	160
Glu	Lys	Asn	Val	Val	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Asp	Ile	165	170	175	
Tyr	Lys	Asp	Pro	Asp	Tyr	Val	Arg	Lys	Gly	Asp	Ala	Arg	Leu	Pro	Leu	180	185	190	
Lys	Trp	Met	Ala	Pro	Glu	Thr	Ile	Phe	Asp	Arg	Val	Tyr	Thr	Ile	Gln	195	200	205	
Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Leu	Leu	Trp	Glu	Ile	Phe	Ser	Leu	210	215	220	
Gly	Ala	Ser	Pro	Tyr	Pro	Gly	Val	Lys	Ile	Asp	Glu	Glu	Phe	Cys	Arg	225	230	235	240
Arg	Leu	Lys	Glu	Gly	Thr	Arg	Met	Arg	Ala	Pro	Asp	Tyr	Thr	Thr	Pro	245	250	255	

Glu Met Tyr Gln Thr Met Leu Asp Cys Trp His Gly Glu Pro Ser Gln
260 265 270

Arg Pro Thr Phe Ser Glu Leu Val Glu His Leu Gly Asn Leu Leu Gln
275 280 285

Ala Asn Ala
290

<210> 17

<211> 290

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: FGFR1 tyrosine kinase
sequence

<400> 17

Glu Leu Pro Arg Asp Arg Leu Val Leu Gly Lys Pro Leu Gly Glu Gly
1 5 10 15

Ala Phe Gly Gln Val Val Leu Ala Glu Ala Ile Gly Leu Asp Lys Asp
20 25 30

Lys Pro Asn Arg Val Thr Lys Val Ala Val Lys Met Leu Lys Ser Asp
35 40 45

Ala Thr Glu Lys Asp Leu Ser Asp Leu Ile Ser Glu Met Glu Met Met
50 55 60

Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys
65 70 75 80

Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly
85 90 95

Asn Leu Arg Glu Tyr Leu Gln Ala Arg Arg Pro Pro Gly Leu Glu Tyr
100 105 110

Ser Tyr Asn Pro Ser His Asn Pro Glu Glu Gln Leu Ser Ser Lys Asp
115 120 125

Leu Val Ser Cys Ala Tyr Gln Val Ala Arg Gly Met Glu Tyr Leu Ala
130 135 140

Ser Lys Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu Val
145 150 155 160

Thr Glu Asp Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp
165 170 175

Ile His His Ile Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro
180 185 190

Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Ile Tyr Thr His
 195 200 205

Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Thr
 210 215 220

Leu Gly Gly Ser Pro Tyr Pro Gly Val Pro Val Glu Glu Leu Phe Lys
 225 230 235 240

Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ser Asn Cys Thr Asn
 245 250 255

Glu Leu Tyr Met Met Met Arg Asp Cys Trp His Ala Val Pro Ser Gln
 260 265 270

Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg Ile Val Ala
 275 280 285

Leu Thr
 290

<210> 18
 <211> 294
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: INSR tyrosine kinase
 sequence

<400> 18
 Glu Val Ser Arg Glu Lys Ile Thr Leu Leu Arg Glu Leu Gly Gln Gly
 1 5 10 15

Ser Phe Gly Met Val Tyr Glu Gly Asn Ala Arg Asp Ile Ile Lys Gly
 20 25 30

Glu Ala Glu Thr Arg Val Ala Val Lys Thr Val Asn Glu Ser Ala Ser
 35 40 45

Leu Arg Glu Arg Ile Glu Phe Leu Asn Glu Ala Ser Val Met Lys Gly
 50 55 60

Phe Thr Cys His His Val Val Arg Leu Leu Gly Val Val Ser Lys Gly
 65 70 75 80

Gln Pro Thr Leu Val Val Met Glu Leu Met Ala His Gly Asp Leu Lys
 85 90 95

Ser Tyr Leu Arg Ser Leu Arg Pro Glu Ala Glu Asn Asn Pro Gly Arg
 100 105 110

Pro Pro Pro Thr Leu Gln Glu Met Ile Gln Met Ala Ala Glu Ile Ala
 115 120 125

Asp Gly Met Ala Tyr Leu Asn Ala Lys Lys Phe Val His Arg Asp Leu
 130 135 140
 Ala Ala Arg Asn Cys Met Val Ala His Asp Phe Thr Val Lys Ile Gly
 145 150 155 160
 Asp Phe Gly Met Thr Arg Asp Ile Tyr Glu Thr Asp Tyr Tyr Arg Lys
 165 170 175
 Gly Gly Lys Gly Leu Leu Pro Val Arg Trp Met Ala Pro Glu Ser Leu
 180 185 190
 Lys Asp Gly Val Phe Thr Thr Ser Ser Asp Met Trp Ser Phe Gly Val
 195 200 205
 Val Leu Trp Glu Ile Thr Ser Leu Ala Glu Gln Pro Tyr Gln Gly Leu
 210 215 220
 Ser Asn Glu Gln Val Leu Lys Phe Val Met Asp Gly Gly Tyr Leu Asp
 225 230 235 240
 Gln Pro Asp Asn Cys Pro Glu Arg Val Thr Asp Leu Met Arg Met Cys
 245 250 255
 Trp Gln Phe Asn Pro Lys Met Arg Pro Thr Phe Leu Glu Ile Val Asn
 260 265 270
 Leu Leu Lys Asp Asp Leu His Pro Ser Phe Pro Glu Val Ser Phe Phe
 275 280 285
 His Ser Glu Glu Asn Lys
 290

<210> 19
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 19
 Glu Val Ala Arg Glu Lys Ile Thr Met Ser Arg Glu Leu Gly Gln Gly
 1 5 10 15
 Ser Phe Gly Met Val Tyr Glu Gly Val Ala Lys Gly Val Val Lys Asp
 20 25 30
 Glu Pro Glu Thr Arg Val Ala Ile Lys Thr Val Asn Glu Ala Ala Ser
 35 40 45
 Met Arg Glu Arg Ile Glu Phe Leu Asn Glu Ala Ser Val Met Lys Glu
 50 55 60
 Phe Asn Cys His His Val Val Arg Leu Leu Gly Val Val Ser Gln Gly
 65 70 75 80
 Gln Pro Thr Leu Val Ile Met Glu Leu Met Thr Arg Gly Asp Leu Lys
 85 90 95

Ser Tyr Leu Arg Ser Leu Arg Pro Glu Met Glu Asn Asn Pro Val Leu
 100 105 110
 Ala Pro Pro Ser Leu Ser Lys Met Ile Gln Met Ala Gly Glu Ile Ala
 115 120 125
 Asp Gly Met Ala Tyr Leu Asn Ala Asn Lys Phe Val His Arg Asp Leu
 130 135 140
 Ala Ala Arg Asn Cys Met Val Ala Glu Asp Phe Thr Val Lys Ile Gly
 145 150 155 160
 Asp Phe Gly Met Thr Arg Asp Ile Tyr Glu Thr Asp Tyr Tyr Arg Lys
 165 170 175
 Gly Gly Lys Gly Leu Leu Pro Val Arg Trp Met Ser Pro Glu Ser Leu
 180 185 190
 Lys Asp Gly Val Phe Thr Thr Tyr Ser Asp Val Trp Ser Phe Gly Val
 195 200 205
 Val Leu Trp Glu Ile Ala Thr Leu Ala Glu Gln Pro Tyr Gln Gly Leu
 210 215 220
 Ser Asn Glu Gln Val Leu Arg Phe Val Met Glu Gly Gly Leu Leu Asp
 225 230 235 240
 Lys Pro Asp Asn Cys Pro Asp Met Leu Leu Glu Leu Met Arg Met Cys
 245 250 255
 Trp Gln Tyr Asn Pro Lys Met Arg Pro Ser Phe Leu Glu Ile Ile Ser
 260 265 270
 Ser Ile Lys Glu Glu Met Glu Pro Gly Phe Arg Glu Val Ser Phe Tyr
 275 280 285
 Tyr Ser Glu Glu Asn Lys
 290

<210> 20

<211> 278

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: EPHB2 tyrosine kinase
sequence

<400> 20

Glu Ile Asp Ile Ser Cys Val Lys Ile Glu Gln Val Ile Gly Ala Gly
 1 5 10 15

Glu Phe Gly Glu Val Cys Ser Gly His Leu Lys Leu Pro Gly Lys Arg
 20 25 30

Glu Ile Phe Val Ala Ile Lys Thr Leu Lys Ser Gly Tyr Thr Glu Lys
 35 40 45
 Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met Gly Gln Phe Asp
 50 55 60
 His Pro Asn Val Ile His Leu Glu Gly Val Val Thr Lys Ser Thr Pro
 65 70 75 80
 Val Met Ile Ile Thr Glu Phe Met Glu Asn Gly Ser Leu Asp Ser Phe
 85 90 95
 Leu Arg Gln Asn Asp Gly Gln Phe Thr Val Ile Gln Leu Val Gly Met
 100 105 110
 Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asp Met Asn Tyr
 115 120 125
 Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu
 130 135 140
 Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Phe Leu Glu Asp Asp
 145 150 155 160
 Thr Ser Asp Pro Thr Tyr Thr Ser Ala Leu Gly Gly Lys Ile Pro Ile
 165 170 175
 Arg Trp Thr Ala Pro Glu Ala Ile Gln Tyr Arg Lys Phe Thr Ser Ala
 180 185 190
 Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr
 195 200 205
 Gly Glu Arg Pro Tyr Trp Asp Met Thr Asn Gln Asp Val Ile Asn Ala
 210 215 220
 Ile Glu Gln Asp Tyr Arg Leu Pro Pro Pro Met Asp Cys Pro Ser Ala
 225 230 235 240
 Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Asp Arg Asn His Arg
 245 250 255
 Pro Lys Phe Gly Gln Ile Val Asn Thr Leu Asp Lys Met Ile Arg Asn
 260 265 270
 Pro Asn Ser Leu Lys Ala
 275

<210> 21

<211> 283

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: EGFR tyrosine kinase
sequence

<400> 21

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Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser Gly
 1              5              10              15

Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu Lys
              20              25              30

Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser Pro
      35              40              45

Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser Val
      50              55              60

Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr
      65              70              75              80

Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp Tyr
              85              90              95

Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn Trp
      100              105              110

Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg Leu
      115              120              125

Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro Gln
      130              135              140

His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala Glu
      145              150              155              160

Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp Met
      165              170              175

Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp Val
      180              185              190

Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser Lys
      195              200              205

Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu Lys
      210              215              220

Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr Met
      225              230              235              240

Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys Phe
      245              250              255

Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln Arg
      260              265              270

Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His
      275              280

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<210> 22
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 6-His tag

 <400> 22
 His His His His His His
 1 5

 <210> 23
 <211> 8
 <212> PRT
 <213> Homo sapiens

 <400> 23
 Asp Ile Tyr Ala Glu Ile Pro Asp
 1 5

 <210> 24
 <211> 4
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 pET15S peptide fragment

 <400> 24
 Gly Ser His Met
 1

 <210> 25
 <211> 7
 <212> PRT
 <213> Homo sapiens

 <400> 25
 Ile Tyr Ala Glu Ile Pro Asp
 1 5